

=> d his

(FILE 'HOME' ENTERED AT 11:12:55 ON 16 SEP 2004)

FILE 'AGRICOLA, CAPLUS, BIOSIS' ENTERED AT 11:13:28 ON 16 SEP 2004
ACT DAI307/A

```

L1 (      307)SEA FILE=CAPLUS ABB=ON  PLU=ON  (PIN? OR PROTEINASE INHIBIT?) (6
L2 (      52)SEA FILE=CAPLUS ABB=ON  PLU=ON  L1 AND (POTATO OR SOLANUM OR IP
L3 (      10)SEA FILE=CAPLUS ABB=ON  PLU=ON  L2 AND (SEQUENCE OR DNA OR NUCL
L4 (       0)SEA FILE=AGRICOLA ABB=ON  PLU=ON  L2 AND (SEQUENCE OR DNA OR NU
L5 (       3)SEA FILE=BIOSIS ABB=ON  PLU=ON  L2 AND (SEQUENCE OR DNA OR NUCL
L6      10 DUP REM L3 L4 L5 (3 DUPLICATES REMOVED)

```

=> d ibib abs total 16

L6 ANSWER 1 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN
 ACCESSION NUMBER: 2002:575255 CAPLUS
 DOCUMENT NUMBER: 137:151118
 TITLE: Gene **promoters** of putative
proteinase inhibitor and
 aminotransferase **isolated** from
potato and use thereof
 INVENTOR(S): Dai, Ziyu; Shi, Lifang; Hooker, Brian S.
 PATENT ASSIGNEE(S): USA
 SOURCE: PCT Int. Appl., 43 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002059333	A2	20020801	WO 2002-US1287	20020118
WO 2002059333	C2	20021128		
WO 2002059333	A3	20040212		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2002170095	A1	20021114	US 2002-51307	20020122

PRIORITY APPLN. INFO.: US 2001-263224P P 20010123

AB There are disclosed novel **pin1** gene **promoter** isoforms and amt gene **promoter** isoforms. The two gene promoters as well as their cDNAs are cloned from a cDNA library **isolated** from dark-treated excised **potato** leaf tissues. Gene **pin1** is highly homologous to a tomato ethylene responsive proteinase inhibitor I (er1) gene; while gene amt is highly homologous to capsicum Chinese strain habanero putative aminotransferase cDNA. The described promoters confer light/dark sensitivity and are responsive to ethylene activation. The

promoters and their functional elements may be used independently or in combination with one or more enhancer elements to increase or otherwise manipulate gene expression. The promoters disclosed may be used in Controlled Environment Agriculture (CEA) for heterologous protein production. Also disclosed are methods for using the promoter and promoter elements of the instant invention, as well as vectors and transgenic plants comprising the same.

L6 ANSWER 2 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

ACCESSION NUMBER: 2002:528760 CAPLUS

DOCUMENT NUMBER: 137:363919

TITLE: Targeted expression of human serum albumin to **potato** tubers

AUTHOR(S): Farran, Inma; Sanchez-Serrano, Jose J.; Medina, Juan F.; Prieto, Jesus; Mingo-Castel, Angel M.

CORPORATE SOURCE: Institute of Agrobiotechnology CSIC, Agricultural Production Dept. UPNA, Pamplona, 31006, Spain

SOURCE: Transgenic Research (2002), 11(4), 337-346

CODEN: TRSEES; ISSN: 0962-8819

PUBLISHER: Kluwer Academic Publishers

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Complementary DNA expression of mature human serum albumin was engineered into **potato** plants under the transcriptional control of patatin B33 **promoter** and **potato proteinase inhibitor** II terminator. Protein secretion was achieved by using the signal **sequence** from **potato** proteinase inhibitor II. Recombinant albumin accumulated up to 0.2% of total soluble tuber protein in single transformant lines, regardless of the **potato** cultivar used. Electrophoretic mobility and N-terminal amino acid **sequence** anal. of partially **purified** recombinant albumin confirmed proper processing of an immune responsive recombinant albumin, and revealed that the proteinase inhibitor II signal **sequence** was correctly removed. No further optimization of these yields was obtained by HSA expression in patatin antisense plants (line Pas58). Subcellular localization showed that recombinant protein was successfully targeted to the apoplast. **Potato** tubers may be used, by applying this technol., to produce other heterologous proteins of interest in the biopharmaceutical industry.

REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 3 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1998:509301 CAPLUS

DOCUMENT NUMBER: 129:132211

TITLE: Nematode infection-induced plant promoters from *Arabidopsis thaliana*

INVENTOR(S): Karimi, Mansour; Barthels, Nathalie; Gheysen, Godelieve

PATENT ASSIGNEE(S): Plant Genetic Systems, N.V., Belg.

SOURCE: PCT Int. Appl., 56 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
-----	----	-----	-----	-----

WO 9831822 A1 19980723 WO 1998-EP388 19980119
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG,
KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,
NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT,
UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI,
FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM,
GA, GN, ML, MR, NE, SN, TD, TG
AU 9866157 A1 19980807 AU 1998-66157 19980119
AU 720780 B2 20000615
BR 9807488 A 20000321 BR 1998-7488 19980119
EP 1007709 A1 20000614 EP 1998-907984 19980119
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO
JP 2001508661 T2 20010703 JP 1998-533700 19980119
US 6252138 B1 20010626 US 1999-341678 19990720
PRIORITY APPLN. INFO.: EP 1997-200103 A 19970120
WO 1998-EP388 W 19980119

AB New pathogen-induced promoters are provided, particularly nematode-induced promoters, which are characterized by their selective induction of expression in the vicinity of the pathogen infection sites, such as the fixed feeding cells induced by infection of the plant by nematodes. T-DNA tagging with pAgusBin19 was used for the identification of a promoter induced by nematode inoculation (*Heterodera schachtii*, *Meloidogyne incognita*, or *Xiphinema diversicaudatum*) in an early stage of *Arabidopsis thaliana* line ARM1. PCR amplified fragments of the T-DNA insertion sites are used as a probe to screen a genomic library of DNA of a wild-type *A. thaliana* line to isolate genomic clones carrying the uninterrupted genomic DNA of the wild-type line C24 which is the target sequence for T-DNA integration in line ARM1. Deletion anal. identified regions that confer more specific and/or more enhanced promoter activity when combined with either homologous or heterologous transcription signals such as TATA-boxes or upstream enhancing elements. Further provided are chimeric genes comprising these promoters as regulatory elements, as well as transgenic plants, comprising those chimeric genes, which are less susceptible to pathogen infections. Chimeric genes carrying a barnase coding region or a proteinase inhibitor coding region (oryzacystatin-I) under control of the nematode-inducible promoter cause resistance to nematode infection in transformed potato or oilseed rape plants.

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 4 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 2
ACCESSION NUMBER: 1997:630022 CAPLUS
DOCUMENT NUMBER: 127:288776
TITLE: T7 RNA polymerase is expressed in plants in a nicked but active form
AUTHOR(S): Caviedes, Miguel A.; Park, Sanggyu; Thornburg, Robert W.
CORPORATE SOURCE: Dep. Microbiol. Parasitology, Univ. Sevilla, Spain
SOURCE: Han'guk Nonghwa Hakhoechi (1997), 40(4), 271-276
CODEN: JKACA7; ISSN: 0368-2897
PUBLISHER: Korean Society of Agricultural Chemistry and Biotechnology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Several chimeric constructs containing the bacteriophage T7 RNA polymerase

gene under control of the wound-inducible **potato proteinase inhibitor II (pin2)** **promoter** were prepared, and *Nicotiana tabacum* plants were transformed with these constructs. Southern blot analyses indicate that either one or two copies of the gene constructs are present in the transgenic plants. Northern blot analyses indicate that mRNA encoding T7 RNA polymerase is expressed in a wound-inducible manner. T7 RNA polymerase was **purified** and antiserum was prepared. This antiserum was used for Western blot analyses to demonstrate that a protein which is cross reactive with T7 RNA polymerase is produced. The mol. mass of this protein is 80 kDa, a size which is consistent with the nicked form of the polymerase as is often seen when expressed in *E. coli*. RNA polymerase assays were used to indicate that the nicked form of T7 RNA polymerase is active and capable of incorporating labeled **nucleotides** into transcripts in vitro. Anal. of transgenic plants did indeed show that wound-inducible activation of the T7 RNA polymerase permits the establishment of a genetic system to overexpress genes in plants using T7 RNA polymerase.

REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1997:169943 CAPLUS

DOCUMENT NUMBER: 126:167267

TITLE: **Isolation** and structural analysis of the 5'-upstream **promoter** region of an aspartic **proteinase inhibitor** gene from **potato**

AUTHOR(S): Liu, Zhongda; Hu, Tingmao; Wang, Yongsheng

CORPORATE SOURCE: Dep. Mol. Biol., NeiMonggol Univ., Hohhot, 010021, Peop. Rep. China

SOURCE: Neimenggu Daxue Xuebao, Ziran Kexueban (1996), 27(4), 573-576

CODEN: NDZKEJ; ISSN: 1000-1638

PUBLISHER: Neimenggu Daxue Xuebao Bianjibu

DOCUMENT TYPE: Journal

LANGUAGE: Chinese

AB A **DNA** fragment containing the 5'-upstream region of an aspartic proteinase inhibitor gene was **isolated** from **potato** total **DNA** by single-specific-primer polymerase chain reaction (ssp-PCR). The **DNA** fragment was cloned into the SmaI site of the pUC18 vector. One promoter pos. clone was obtained. Typical CAAT and TATA box-like **sequences** were found in the insert containing the 5'-upstream region of an aspartic proteinase inhibitor gene.

L6 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 3

ACCESSION NUMBER: 1996:515315 CAPLUS

DOCUMENT NUMBER: 125:187109

TITLE: Loss of specific **sequences** in a natural variant of **potato** proteinase inhibitor II gene results in a loss of wound-inducible gene expression

AUTHOR(S): Park, Sanggyu; Thornburg, Robert W.

CORPORATE SOURCE: Dep. Agric. Chem., Taegu Univ., S. Korea

SOURCE: Han'guk Nonghwa Hakhoechi (1996), 39(2), 104-111

CODEN: JKACA7; ISSN: 0368-2897

PUBLISHER: Korean Society of Agricultural Chemistry and Biotechnology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB We have **isolated** several proteinase inhibitor II genes **pin2** from a Russet Burbank **potato DNA** library. One of these **pin2T** was subcloned and a 1.8 kb **XbaI/NsiI** insert was sequenced. This fragment contained the complete Inhibitor II gene including 965 bp of flanking **DNA** upstream from the gene and 200bp of flanking **DNA** downstream from the gene. The open reading frame encodes a protein that is similar to other reported proteinase Inhibitor II proteins. The **DNA sequence** of the 5' flanking region of **pin2T** from -714 to +1 is highly homologous (91% identity) with that of the previously **isolated** wound-inducible **pin2K**. There are, however, four small deletions in the **pin2T promoter** which are located at -221 to -200, -263 to -254, -523 to -426 and -759 to -708 relative to the transcription start site of the wound-inducible **pin2K**. Three of these deletions map to a portion of the promoter that controls the wound-inducibility of the proteinase inhibitor genes. Chimeric genes containing the **promoter** of the **pin2T** gene linked with the both **CAT** and **GUS** were constructed and transferred into tobacco plants. Anal. of these plants indicated that **pin2T** is not a wound-inducible gene but is expressed at low levels. Thus, wound-inducibility is lost with the concomitant natural deletion of three small regions of the promoter. Comparison of the **sequences** deleted in **pin2T** relative to the **pin2K** with Genebank **sequences** indicates that the deleted **sequences** contain a motif (consensus 5'-AGTAAA-3') that is found in many other wound-inducible genes but not easily found in the published promoter **sequences** of other plant genes. Nuclear proteins from unwounded and wounded **potato** leaves were bound to the proximal promoter region, downstream of the 5'-AGTAAA-3', of **pin2T**. The comparison of the **pin2T** gene with the **pin2K** gene indicates that the natural internal **promoter** deletions are likely responsible for loss of the wound-inducible phenotype in the **pin2T** gene.

L6 ANSWER 7 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1995:172689 CAPLUS

DOCUMENT NUMBER: 122:26156

TITLE: Posttranslational modification of an isoinhibitor from the **potato** proteinase inhibitor II gene family in transgenic tobacco yields a peptide with homology to **potato** chymotrypsin inhibitor I

AUTHOR(S): McManus, Michael T.; Laing, William A.; Christeller, John T.; White, Derek W. R.

CORPORATE SOURCE: Plant Mol. Genet. Lab., Grasslands Res. Cent., Palmerston North, N. Z.

SOURCE: Plant Physiology (1994), 106(2), 771-7

CODEN: PLPHAY; ISSN: 0032-0889

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A member of the **potato** proteinase inhibitor II (PPI-II) gene family under the control of the cauliflower mosaic virus 35S promoter has been introduced into tobacco (*Nicotiana tabacum*). **Purifn.** of the PPI-II protein that accumulates in transgenic tobacco has confirmed that the N-terminal signal **sequence** is removed and that the inhibitor accumulates as a protein of the expected size (21 kD). However, a smaller peptide of approx. 5.4 kD has also been identified as a foreign gene product in transgenic tobacco plants. This peptide is recognized by an anti-PPI-II antibody, inhibits the serine proteinase chymotrypsin, and is not observed in nontransgenic tobacco. Furthermore, amino acid sequencing demonstrates that the peptide is identical to a lower mol. weight

chymotrypsin inhibitor found in **potato** tubers and designated as **potato** chymotrypsin inhibitor I (PCI-I). Together, these data confirm that, as postulated to occur in **potato**, PCI-I does arise from the full-length PPI-II protein by posttranslational processing. The use of transgenic tobacco represents an ideal system with which to determine the precise mechanism by which this protein modification occurs.

L6 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1993:442348 CAPLUS

DOCUMENT NUMBER: 119:42348

TITLE: **Isolation and sequence analysis of the genomic DNA fragment encoding an aspartic proteinase inhibitor homolog from potato (Solanum tuberosum L.)**

AUTHOR(S): Barlic Maganja, Darja; Strukelj, Borut; Pungercar, Joze; Gubensek, Franc; Turk, Vito; Kregar, Igor

CORPORATE SOURCE: Dep. Biochem., Jozef Stefan Inst., Ljubljana, 61000, Slovenia

SOURCE: Plant Molecular Biology (1992), 20(2), 311-13

CODEN: PMBIDB; ISSN: 0167-4412

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A genomic **DNA** clone encoding an aspartic proteinase of **potato** was **isolated** from a lambda EMBL3 phage library using the aspartic proteinase inhibitor cDNA as a hybridization probe. The gene has all characteristic **sequences** normally found in eukaryotic genes. Typical CAAT and TATA box **sequences** were found in the 5'-upstream region. In this part two putative regulatory AGGA box **sequences** are also located. In the genomic **sequence** there are no intron **sequences** interrupting the coding region. An open reading frame of the gene encodes a precursor protein of 217 amino acids which shows high percent identity with the aspartic proteinase inhibitor cDNA.

L6 ANSWER 9 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1990:606230 CAPLUS

DOCUMENT NUMBER: 113:206230

TITLE: Plant expression vectors using a promoter from a wound-inducible gene from **potato**

INVENTOR(S): Keil, Michael; Sanchez-Serrano, Jose; Willmitzer, Lothar

PATENT ASSIGNEE(S): Institut fuer Genbiologische Forschung Berlin G.m.b.H., Germany

SOURCE: Eur. Pat. Appl., 14 pp.

CODEN: EPXXDW

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 375091	A1	19900627	EP 1989-250116	19891218
R: AT, BE, CH, DE, ES, FR, GB, GR, IT, LI, LU, NL, SE				
DE 3843628	A1	19900705	DE 1988-3843628	19881221
DK 8906514	A	19900622	DK 1989-6514	19891220
JP 02283275	A2	19901120	JP 1989-329771	19891221
CA 2007091	AA	19910703	CA 1990-2007091	19900103
PRIORITY APPLN. INFO.:			DE 1988-3843628	19881221

AB The gene for proteinase inhibitor II of **potato** is cloned and the promoter and transcription terminator used in expression cassettes for regulated gene expression in leaves and stems and constitute expression in **potato** tubers. The genomic clone was **isolated** from a genomic bank using a cDNA clone as probe. The regions required from wound-inducibility were identified by deletion anal., using expression in transgenic tobacco of a CAT (chloramphenicol transacetylase) gene as the assay. The intron in the coding **sequence** of the inhibitor gene was shown not be involved in regulation of expression. Expts. using an inactivated CaMV 35S promoter showed that this promoter could be activated by the inhibitor gene promoter and that the gene promoter had enhanced activity. The proteinase inhibitor expression cassette was used to express a barley thionin gene in tobacco (no data).

L6 ANSWER 10 OF 10 CAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 1991:18435 CAPLUS

DOCUMENT NUMBER: 114:18435

TITLE: **Nucleotide sequence** of a proteinase inhibitor I gene in **potato**

AUTHOR(S): Lee, Jong Seob; Park, Jung Sook

CORPORATE SOURCE: S. Korea

SOURCE: Sikmul Hakhoechi (1989), 32(2), 67-78

CODEN: KJBOAI; ISSN: 0583-421X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Hybridization of **DNA isolated** from leaves of Russet Burbank **potato** with a tomato cDNA probe revealed the presence of about ten proteinase inhibitor I genes in the genome. Screening of a genomic library of Russet Burbank **potato** resulted in **isolation** of 7 different genomic clones carrying inhibitor I genes. One of the genomic clones, clone 2, contained 2 EcoRI fragments of 3.4 and 1.8 kb in size, resp., which hybridized with the probe. The **nucleotide sequence** of portions of the hybridizing EcoRI fragments revealed that they contain a complete gene which codes for an open reading frame of 107 amino acids. It is interrupted by 2 intervening **sequences** of 502 and 493 bp, situated at the positions of codons 17 and 43, resp., of the open reading frame. Putative regulatory **sequences**, TATAAA and CCACT, were found at the 5' flanking region. In addition, a copy of a 100 bp repeat found in a tomato inhibitor I gene was identified.

=>